



SEQUENCE LISTING

<110> Andersson, Leif
Luthman, L. Holger
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#6

<120> VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT

<130> 11145-007001

<140> US 09/826,581

<141> 2001-04-05

<150> US 60/195,665

<151> 2000-04-07

<160> 14

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 821

<212> DNA

<213> Homo sapiens

<400> 1

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| tctgagagcc | caactctgct | caatgaccat | gttcccacat | gctccaagcc | acatcccctc | 60 |
| aaaaagggtc | cctctagctt | gtcctcagtg | accagaggag | cagctgagga | ccaagtaccc | 120 |
| agattatccg | gtgcgcccct | tccctcccag | caacccccag | ccttcagggc | tgtagcagct | 180 |
| gagcaaattg | gggcccctcc | ctctcattgc | ctgacaccca | atcagagaga | aaccgatcct | 240 |
| ggcagggcag | ggtgcccggg | gccgggcccc | gaatagtgca | gcccagccac | agtgtcgcac | 300 |
| acttgctctc | agttggtctg | gggctggcca | catggagccc | gggctggagc | acgcactgcg | 360 |
| cagggatatg | gggtcccagg | ggagccggag | ccggggcagc | tgaggccaga | agattgagcg | 420 |
| cacgggctgt | gaatgtgtgt | gtgggcgtgt | gtgtcttctg | gtgtgtgttt | ggtctggatt | 480 |
| ttctcgtgaa | tatgggcatg | tgcattgttt | ggcatatgta | ttgtgagtgt | gtgtggttct | 540 |
| gtgtgccttg | gagtgttttg | atgtgtgtgt | ttctgtgtgt | gtttgtgtat | ggctgcattg | 600 |
| ctgtgtatgg | cgtgtgtctg | agcgtgtgta | ttgggtgtgca | tgggtgtgta | ggcgtgtggt | 660 |
| cagggagaag | gggtttggga | atgtaaggca | ctttccccac | tccttcagaa | actcttctcc | 720 |
| ccacagaccc | cttctctggg | cagccttggg | ggttctgagc | atcaaggtag | ggagaatgcc | 780 |
| ccctccctgg | ggcctaacct | cttcccccac | ttccttgctc | c | | 821 |

<210> 2

<211> 989

<212> DNA

<213> Homo sapiens

<400> 2

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| caggccccat | tccccttcca | gagatgagct | tcttagagca | agaaaacagc | agctcatggc | 60 |
| catcaccagc | tgtgaccagc | agctcagaaa | gaatccgtgg | gaaacggagg | gccaaagcct | 120 |
| tgagatggac | aaggcagaag | tgggtggagg | aaggggagcc | accaggtcag | ggggaagggtg | 180 |
| aggccaaggc | cagttctggg | gaggtgggag | ccaggggagt | gggaaatccc | agaggagcct | 240 |
| gggtctggtc | tctacctcag | gtccctccat | aacacagagt | tggacccaac | cttcattctg | 300 |
| tggcctcagt | ctccctacat | agtagagaac | aaggcactgc | agtgccagag | gccagcatgg | 360 |

| | | | | | | |
|-------------|------------|-------------|------------|-------------|-------------|-----|
| ccaactcaga | aagatgggac | agagccacta | cctggggcga | ctctcaggtc | agccccctcac | 420 |
| ctgcaaatag | ggccacagca | tccaggcttc | ccactgctgc | tgtgagatga | atggcgacag | 480 |
| cagatgagaa | cgtgcttttg | aagatggagt | tactgtcctc | ttccccctcct | cccccaaaca | 540 |
| ggtccccggt | ccaggccagc | tgctgagtc | accgggctgg | aggccacatt | ccccaaagacc | 600 |
| acacccttgg | ctcaagctga | tccctgccggg | gtgggcactc | caccaacagg | gtgggactgc | 660 |
| ctccccctctg | actgtacagc | ctcagctgca | ggctccagca | cagatgatgt | ggagctggcc | 720 |
| acggagttcc | cagccacaga | ggcctgggag | tgtgagctag | aaggcctgct | ggaagagagg | 780 |
| cctgccctgt | gcctgtcccc | gcaggcccca | tttcccaagc | tgggctggga | tgacgaactg | 840 |
| cggaaacccg | gcgcccagat | ctacatgcgc | ttcatgcagg | agcacacctg | ctacgatgcc | 900 |
| atggcaacta | gctccaagct | agtcattcttc | gacaccatgc | tggaggtgag | gccacggctc | 960 |
| tgcccaacct | gtactcactc | tccatccac | | | | 989 |

<210> 3

<211> 1722

<212> DNA

<213> Homo sapiens

<400> 3

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| cctggccccct | cagatcaaga | aggccttctt | tgtcttggtg | gccaacggtg | tgccgggcagc | 60 |
| ccctctatgg | gacagcaaga | agcagagctt | tgtgggtgag | gagaggctgg | ggaggtgaag | 120 |
| ggagatggag | gaggtgaggg | ggagatcttg | tacggttggt | ctggggctga | tctctgatat | 180 |
| accacaagct | tggcttcagg | ccaagcccag | ccaggggcca | gggtggagga | aagtccatcc | 240 |
| ggagtctgca | tggccagctg | ggagaccctg | gggtcaatt | tccccatctg | tggagccgct | 300 |
| atgaccagct | gacacctttc | acctccgcta | ctgcatggcc | ctgtgccata | ggtgctaggg | 360 |
| agcaaatggg | gggaggcagg | agagaaagag | ccccacttct | caggcctggg | gggtgcccc | 420 |
| actgtcctgt | tcccacagtc | cccactgtgt | ctcagcacia | ggacactggc | aggggtggga | 480 |
| gggatctga | ccctcaacct | gccttccacc | caaaggcccc | gggtgacct | cctccccgcc | 540 |
| cctccccctgc | agggatgctg | accatcactg | acttcactct | ggtgctgcat | cgctactaca | 600 |
| ggtccccccct | ggtgaggagt | gggtgggaa | tcttatgggc | accagagggg | gcgggggcgg | 660 |
| aggggagtcc | tcttgagacc | tgggtgcccta | gaagcccacg | tctttctgac | ttctggagtc | 720 |
| ctgtcagatg | ctctaggctc | agatctatga | gattgaacaa | cataagattg | agacctggag | 780 |
| gggtgagtgg | ggagaggaac | ccggaaaggg | gctgttggtg | atggtgggcc | agggcttaag | 840 |
| gtggaggatg | ggcagtgggg | atgtcctgga | gtgaacaggg | gagggacaat | aggagcctcg | 900 |
| ggtgcctgac | ggaagggaag | ctgcctggga | ctgcaagggtg | aggcagggtga | ccggctcccc | 960 |
| tggcctgact | ctggctcttt | ctgcagagat | ctacctgcaa | ggctgcttca | agcctctggt | 1020 |
| ctccatctct | cctaattgata | ggtgggtgtc | tctgctcatt | cacctgagcc | tcctcctccc | 1080 |
| acagtccccct | tccccagtc | cactcagctc | tgaactcacc | tcttcactct | aggcggcaca | 1140 |
| cagacaaggg | agccttggtg | ccctgccctc | ctttttaggg | gcctgggatg | gaggttgtct | 1200 |
| ctccctaggc | tgccccgagg | ctcactgctc | ccatctctgc | agcctgtttg | aagctgtcta | 1260 |
| caccctcatc | aagaaccgga | tccatgcct | gcctgttctt | gacccgggtg | caggcaacgt | 1320 |
| actccacatc | ctcacacaca | aacgcctgct | caagtccctg | cacatctttg | taagcctggg | 1380 |
| cccagggtggg | aggaaggggg | agacctgggc | aggtgatcag | agggcctgag | gagtcttcag | 1440 |
| ccctagcagt | cgtggggaag | agctgggagc | cctcttgaag | ctgctggatc | cctgatctcc | 1500 |
| acctggtccc | catactaacc | agggttccct | gctgccccgg | ccctccttcc | tctaccgcac | 1560 |
| tatccaagat | ttgggcatcg | gcacattccg | agacttggct | gtggtgctgg | agacagcacc | 1620 |
| catcctgact | gcactggaca | tctttgtgga | ccggcggtgtg | tctgcactgc | ctgtggtcaa | 1680 |
| cgaatgtggt | acccaccccc | aggatgagag | gctcgggctg | ga | | 1722 |

<210> 4

<211> 1014

<212> DNA

<213> Homo sapiens

<400> 4

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cctgtctttc tccccccacc ccccaacaacc accctctgca ggtcagggtcg tgggcctcta      60
ttcccgcctt gatgtgattg taagtgtcgc tggaaagggtg ggatgctgca gggagggctaa      120
gggtgtgggg atgggtgggg ggccctctgtg gaccaggggg accttgacaa gtatgcaggg      180
gttgacatct gtagggtagg agcccaggca aggggggtgac taggagccat acttctctct      240
ctgccccagc acctggctgc ccagcaaacc tacaaccacc tggacatgag tgtggggagaa      300
gccctgaggc agaggacact atgtctggag ggagtccttt cctgccagcc ccacgagagc      360
ttgggggaag tgatcgacag gattgctcgg gagcagggtac cgtgtgccct ccattcatgc      420
ccccaacaca tatagcccag tccttctcat gcacggctcc agccatccct gaacatcggg      480
cacctggcct atccttccat ttcatgacca actcctgggtg cccacactgg cctgcacctg      540
gtcctgtcca tggggccctt atgccagggg tccactgcca ctgatcacct taggccgggtc      600
acaccatccc taactggttt ctaggagacg ctctctccct cagtcatgtt gggttgtttc      660
ccctgattct tggcaccaac ctacgtagct gctgtagccc catggctctg cccctcact      720
gaacattgcg gaccacaggg tacacaggct ggtgctagtg gacgagaccc agcatctctt      780
gggcgtggtc tccctctccg acatccttca ggcactgggtg ctacgccctg ctggcatcga      840
tgccctcggg gcctgagaag atctgagtc tcaatcccaa gccacctgca cacctggaag      900
ccaatgaagg gaactggaga actcagcctt catcttcccc caccctcatt tgctgtgtca      960
gctatgattc aggtaggctc tgccctgggc catgacacca gcctcttagt cttc      1014

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<210> 5

<211> 1647

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (20) ... (1486)

<400> 5

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ttgggtctggg gctggccac atg gag ccc ggg ctg gag cac gca ctg cgc agg      52
          Met Glu Pro Gly Leu Glu His Ala Leu Arg Arg
                   1                   5                   10

acc cct tcc tgg agc agc ctt ggg ggt tct gag cat caa gag atg agc      100
Thr Pro Ser Trp Ser Ser Leu Gly Gly Ser Glu His Gln Glu Met Ser
                   15                   20                   25

ttc cta gag caa gaa aac agc agc tca tgg cca tca cca gct gtg acc      148
Phe Leu Glu Gln Glu Asn Ser Ser Ser Trp Pro Ser Pro Ala Val Thr
                   30                   35                   40

agc agc tca gaa aga atc cgt ggg aaa cgg agg gcc aaa gcc ttg aga      196
Ser Ser Ser Glu Arg Ile Arg Gly Lys Arg Arg Ala Lys Ala Leu Arg
                   45                   50                   55

tgg aca agg cag aag tcg gtg gag gaa ggg gag cca cca ggt cag ggg      244
Trp Thr Arg Gln Lys Ser Val Glu Glu Gly Glu Pro Pro Gly Gln Gly
                   60                   65                   70                   75

gaa ggt ccc cgg tcc agg cca gct gct gag tcc acc ggg ctg gag gcc      292
Glu Gly Pro Arg Ser Arg Pro Ala Ala Glu Ser Thr Gly Leu Glu Ala
                   80                   85                   90

```

| | |
|---|-----|
| aca ttc ccc aag acc aca ccc ttg gct caa gct gat cct gcc ggg gtg Thr Phe Pro Lys Thr Thr Pro Leu Ala Gln Ala Asp Pro Ala Gly Val 95 100 105 | 340 |
| ggc act cca cca aca ggg tgg gac tgc ctc ccc tct gac tgt aca gcc Gly Thr Pro Pro Thr Gly Trp Asp Cys Leu Pro Ser Asp Cys Thr Ala 110 115 120 | 388 |
| tca gct gca ggc tcc agc aca gat gat gtg gag ctg gcc acg gag ttc Ser Ala Ala Gly Ser Ser Thr Asp Asp Val Glu Leu Ala Thr Glu Phe 125 130 135 | 436 |
| cca gcc aca gag gcc tgg gag tgt gag cta gaa ggc ctg ctg gaa gag Pro Ala Thr Glu Ala Trp Glu Cys Glu Leu Glu Gly Leu Leu Glu Glu 140 145 150 155 | 484 |
| agg cct gcc ctg tgc ctg tcc ccg cag gcc cca ttt ccc aag ctg ggc Arg Pro Ala Leu Cys Leu Ser Pro Gln Ala Pro Phe Pro Lys Leu Gly 160 165 170 | 532 |
| tgg gat gac gaa ctg cgg aaa ccc ggc gcc cag atc tac atg cgc ttc Trp Asp Asp Glu Leu Arg Lys Pro Gly Ala Gln Ile Tyr Met Arg Phe 175 180 185 | 580 |
| atg cag gag cac acc tgc tac gat gcc atg gca act agc tcc aag cta Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser Lys Leu 190 195 200 | 628 |
| gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt gct ctg Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe Ala Leu 205 210 215 | 676 |
| gtg gcc aac ggt gtg cgg gca gcc cct cta tgg gac agc aag aag cag Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys Lys Gln 220 225 230 235 | 724 |
| agc ttt gtg ggg atg ctg acc atc act gac ttc atc ctg gtg ctg cat Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val Leu His 240 245 250 | 772 |
| cgc tac tac agg tcc ccc ctg gtc cag atc tat gag att gaa caa cat Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu Gln His 255 260 265 | 820 |
| aag att gag acc tgg agg gag atc tac ctg caa ggc tgc ttc aag cct Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe Lys Pro 270 275 280 | 868 |
| ctg gtc tcc atc tct cct aat gat agc ctg ttt gaa gct gtc tac acc Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val Tyr Thr 285 290 295 | 916 |
| ctc atc aag aac cgg atc cat cgc ctg cct gtt ctt gac ccg gtg tca | 964 |

Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro Val Ser
 300 305 310 315
 ggc aac gta ctc cac atc ctc aca cac aaa cgc ctg ctc aag ttc ctg 1012
 Gly Asn Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys Phe Leu
 320 325 330
 cac atc ttt ggt tcc ctg ctg ccc cgg ccc tcc ttc ctc tac cgc act 1060
 His Ile Phe Gly Ser Leu Leu Pro Arg Pro Ser Phe Leu Tyr Arg Thr
 335 340 345
 atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gct gtg gtg ctg 1108
 Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val Val Leu
 350 355 360
 gag aca gca ccc atc ctg act gca ctg gac atc ttt gtg gac cgg cgt 1156
 Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp Arg Arg
 365 370 375
 gtg tct gca ctg cct gtg gtc aac gaa tgt ggt cag gtc gtg ggc ctc 1204
 Val Ser Ala Leu Pro Val Val Asn Glu Cys Gly Gln Val Val Gly Leu
 380 385 390 395
 tat tcc cgc ttt gat gtg att cac ctg gct gcc cag caa acc tac aac 1252
 Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr Tyr Asn
 400 405 410
 cac ctg gac atg agt gtg gga gaa gcc ctg agg cag agg aca cta tgt 1300
 His Leu Asp Met Ser Val Gly Glu Ala Leu Arg Gln Arg Thr Leu Cys
 415 420 425
 ctg gag gga gtc ctt tcc tgc cag ccc cac gag agc ttg ggg gaa gtg 1348
 Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Ser Leu Gly Glu Val
 430 435 440
 atc gac agg att gct cgg gag cag gta cac agg ctg gtg cta gtg gac 1396
 Ile Asp Arg Ile Ala Arg Glu Gln Val His Arg Leu Val Leu Val Asp
 445 450 455
 gag acc cag cat ctc ttg ggc gtg gtc tcc ctc tcc gac atc ctt cag 1444
 Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile Leu Gln
 460 465 470 475
 gca ctg gtg ctc agc cct gct ggc atc gat gcc ctc ggg gcc 1486
 Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
 480 485
 tgagaagatc tgagtctctca atcccaagcc acctgcacac ctggaagcca atgaaggga 1546
 ctggagaact cagccttcat cttccccac cccatttgc tggttcagct atgattcagg 1606
 taggctctgc cctgggccaat gacaccagcc tcttagtctt c 1647

<210> 6

<211> 489

<212> PRT

<213> Homo sapiens

<400> 6

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Met Glu Pro Gly Leu Glu His Ala Leu Arg Arg Thr Pro Ser Trp Ser
 1              5              10              15
Ser Leu Gly Gly Ser Glu His Gln Glu Met Ser Phe Leu Glu Gln Glu
      20              25              30
Asn Ser Ser Ser Trp Pro Ser Pro Ala Val Thr Ser Ser Glu Arg
      35              40              45
Ile Arg Gly Lys Arg Arg Ala Lys Ala Leu Arg Trp Thr Arg Gln Lys
      50              55              60
Ser Val Glu Glu Gly Glu Pro Pro Gly Gln Gly Glu Gly Pro Arg Ser
65              70              75              80
Arg Pro Ala Ala Glu Ser Thr Gly Leu Glu Ala Thr Phe Pro Lys Thr
      85              90              95
Thr Pro Leu Ala Gln Ala Asp Pro Ala Gly Val Gly Thr Pro Pro Thr
      100             105             110
Gly Trp Asp Cys Leu Pro Ser Asp Cys Thr Ala Ser Ala Ala Gly Ser
      115             120             125
Ser Thr Asp Asp Val Glu Leu Ala Thr Glu Phe Pro Ala Thr Glu Ala
      130             135             140
Trp Glu Cys Glu Leu Glu Gly Leu Leu Glu Glu Arg Pro Ala Leu Cys
145             150             155             160
Leu Ser Pro Gln Ala Pro Phe Pro Lys Leu Gly Trp Asp Asp Glu Leu
      165             170             175
Arg Lys Pro Gly Ala Gln Ile Tyr Met Arg Phe Met Gln Glu His Thr
      180             185             190
Cys Tyr Asp Ala Met Ala Thr Ser Ser Lys Leu Val Ile Phe Asp Thr
      195             200             205
Met Leu Glu Ile Lys Lys Ala Phe Phe Ala Leu Val Ala Asn Gly Val
      210             215             220
Arg Ala Ala Pro Leu Trp Asp Ser Lys Lys Gln Ser Phe Val Gly Met
225             230             235             240
Leu Thr Ile Thr Asp Phe Ile Leu Val Leu His Arg Tyr Tyr Arg Ser
      245             250             255
Pro Leu Val Gln Ile Tyr Glu Ile Glu Gln His Lys Ile Glu Thr Trp
      260             265             270
Arg Glu Ile Tyr Leu Gln Gly Cys Phe Lys Pro Leu Val Ser Ile Ser
      275             280             285
Pro Asn Asp Ser Leu Phe Glu Ala Val Tyr Thr Leu Ile Lys Asn Arg
      290             295             300
Ile His Arg Leu Pro Val Leu Asp Pro Val Ser Gly Asn Val Leu His
305             310             315             320
Ile Leu Thr His Lys Arg Leu Leu Lys Phe Leu His Ile Phe Gly Ser
      325             330             335

Leu Leu Pro Arg Pro Ser Phe Leu Tyr Arg Thr Ile Gln Asp Leu Gly
      340             345             350
Ile Gly Thr Phe Arg Asp Leu Ala Val Val Leu Glu Thr Ala Pro Ile
      355             360             365
Leu Thr Ala Leu Asp Ile Phe Val Asp Arg Arg Val Ser Ala Leu Pro
      370             375             380
Val Val Asn Glu Cys Gly Gln Val Val Gly Leu Tyr Ser Arg Phe Asp

```

```

385          390          395          400
Val Ile His Leu Ala Ala Gln Gln Thr Tyr Asn His Leu Asp Met Ser
          405          410          415
Val Gly Glu Ala Leu Arg Gln Arg Thr Leu Cys Leu Glu Gly Val Leu
          420          425          430
Ser Cys Gln Pro His Glu Ser Leu Gly Glu Val Ile Asp Arg Ile Ala
          435          440          445
Arg Glu Gln Val His Arg Leu Val Leu Val Asp Glu Thr Gln His Leu
          450          455          460
Leu Gly Val Val Ser Leu Ser Asp Ile Leu Gln Ala Leu Val Leu Ser
465          470          475          480
Pro Ala Gly Ile Asp Ala Leu Gly Ala
          485

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```

<210> 7
<211> 24
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetically generated primer

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<400> 7
aggctcttgg aataggggct cagg

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24

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<210> 8
<211> 25
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetically generated primer

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<400> 8
agggaattgg ggtcccagaa aagtg

```

25

```

<210> 9
<211> 24
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetically generated primer

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```

<400> 9
gaattgattt tgatgcatta ctcc

```

24

```

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetically generated primer

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<400> 10
agtggcggct gcagcaccgt

20

<210> 11
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<400> 11
aggcagatgg gaggtgcgca ctgag

25

<210> 12
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<400> 12
acagggatgg catgagaaac cctgc

25

<210> 13
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<400> 13
ttctggtagt ggcaccctga tgcaa

25

<210> 14
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<400> 14
gacctgtgag tccttacact tgcag

25